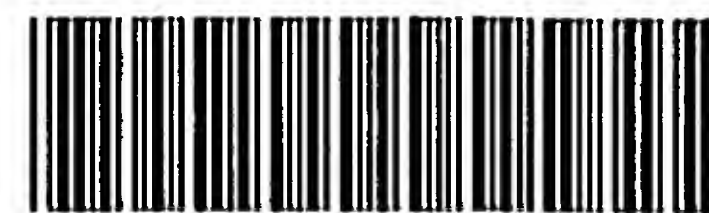# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number:     10/555,407

Source:     PCT

Date Processed by STIC:     11/15/2005

# *ENTERED*

PCT

RAW SEQUENCE LISTING       DATE: 11/15/2005
PATENT APPLICATION:   US/10/555,407     TIME: 10:09:47

Input Set : **A:\SeqListing.txt**
Output Set: **N:\CRF4\11152005\J555407.raw**

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      3 <110> APPLICANT: Dale L. Ludwig
      5 <120> TITLE OF INVENTION: Fully Human Antibodies Directed Against the Human Insulin-
Like
      6        Growth Factor-1 Receptor
      8 <130> FILE REFERENCE: 11245/53202
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/555,407
C--> 11 <141> CURRENT FILING DATE: 2005-11-01
     13 <150> PRIOR APPLICATION NUMBER: PCT/US2004/013852
     14 <151> PRIOR FILING DATE: 2004-05-03
     16 <150> PRIOR APPLICATION NUMBER: US 60/467,177
     17 <151> PRIOR FILING DATE: 2003-05-01
     19 <160> NUMBER OF SEQ ID NOS: 33
     21 <170> SOFTWARE: PatentIn version 3.3
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     24 <211> LENGTH: 390
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Homo sapiens
     29 <220> FEATURE:
     30 <221> NAME/KEY: CDS
     31 <222> LOCATION: (1)..(390)
     33 <400> SEQUENCE: 1
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     35 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
     36 1               5                   10                  15
     38 tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat      96
     39 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
     40                 20                  25                  30
     42 gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg     144
     43 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
     44             35                  40                  45
     46 gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc     192
     47 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
     48         50                  55                  60
     50 cag ggc aga gtc acg att acc gcg gac aaa tcc acg agc aca gcc tac     240
     51 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
     52 65                  70                  75                  80
     54 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt     288
     55 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
     56                 85                  90                  95
     58 gcg aga gcg cca tta cga ttt ttg gag tgg tcc acc caa gac cac tac     336
     59 Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln Asp His Tyr
     60             100                 105                 110
     62 tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc     384
     63 Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
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RAW SEQUENCE LISTING                      DATE: 11/15/2005
PATENT APPLICATION:  US/10/555,407        TIME: 10:09:47

Input Set : A:\SeqListing.txt
Output Set: N:\CRF4\11152005\J555407.raw

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66 tca agc                                                      390
67 Ser Ser
68     130
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72 <211> LENGTH: 130
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 2
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79 1               5                   10                  15
82 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
83             20                  25                  30
86 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
87             35                  40                  45
90 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
91     50                  55                  60
94 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
95 65                  70                  75                  80
98 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
99                 85                  90                  95
102 Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln Asp His Tyr
103             100                 105                 110
106 Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
107             115                 120                 125
110 Ser Ser
111     130
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 1440
116 <212> TYPE: DNA
117 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
121 <221> NAME/KEY: CDS
122 <222> LOCATION: (1)..(1440)
124 <400> SEQUENCE: 3
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127 1               5                   10                  15
129 gta cat tca gag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag      96
130 Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
131             20                  25                  30
133 cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc     144
134 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
135             35                  40                  45
137 agc agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt     192
138 Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
139     50                  55                  60
141 gag tgg atg gga ggg atc atc cct atc ttt ggt aca gca aac tac gca     240
142 Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
```

```
143 65                        70                  75                  80
145 cag aag ttc cag ggc aga gtc acg att acc gcg gac aaa tcc acg agc      288
146 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
147               85                  90                  95
149 aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg      336
150 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
151              100                 105                 110
153 tat tac tgt gcg aga gcg cca tta cga ttt ttg gag tgg tcc acc caa      384
154 Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln
155              115                 120                 125
157 gac cac tac tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg      432
158 Asp His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr
159              130                 135                 140
161 gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg      480
162 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
163 145                 150                 155                 160
165 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc      528
166 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
167              165                 170                 175
169 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca      576
170 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
171              180                 185                 190
173 ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc      624
174 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
175              195                 200                 205
177 tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc      672
178 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
179 210                 215                 220
181 ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac      720
182 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
183 225                 230                 235                 240
185 acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac      768
186 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
187              245                 250                 255
189 aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc      816
190 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
191              260                 265                 270
193 ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc      864
194 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
195              275                 280                 285
197 cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag      912
198 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
199 290                 295                 300
201 gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag      960
202 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
203 305                 310                 315                 320
205 aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc     1008
206 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
207              325                 330                 335
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209 gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag    1056
210 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
211             340                 345                 350
213 tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc    1104
214 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
215             355                 360                 365
217 tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc    1152
218 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
219     370                 375                 380
221 cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg    1200
222 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
223 385                 390                 395                 400
225 gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat    1248
226 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
227             405                 410                 415
229 ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc    1296
230 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
231             420                 425                 430
233 gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg    1344
234 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
235             435                 440                 445
237 tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg    1392
238 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
239     450                 455                 460
241 cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga    1440
242 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
243 465                 470                 475
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 479
248 <212> TYPE: PRT
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 4
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254 1               5                   10                  15
257 Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
258             20                  25                  30
261 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
262         35                  40                  45
265 Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
266     50                  55                  60
269 Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
270 65                  70                  75                  80
273 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
274             85                  90                  95
277 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
278             100                 105                 110
281 Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln
282         115                 120                 125
285 Asp His Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr
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286      130                    135                    140
289 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
290 145                    150                    155                    160
293 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
294                    165                    170                    175
297 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
298                    180                    185                    190
301 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
302                    195                    200                    205
305 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
306                    210                    215                    220
309 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
310 225                    230                    235                    240
313 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
314                    245                    250                    255
317 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
318                    260                    265                    270
321 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
322                    275                    280                    285
325 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
326                    290                    295                    300
329 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
330 305                    310                    315                    320
333 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
334                    325                    330                    335
337 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
338                    340                    345                    350
341 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
342                    355                    360                    365
345 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
346      370                    375                    380
349 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
350 385                    390                    395                    400
353 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
354                    405                    410                    415
357 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
358                    420                    425                    430
361 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
362                    435                    440                    445
365 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
366      450                    455                    460
369 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 465                    470                    475
373 <210> SEQ ID NO: 5
374 <211> LENGTH: 327
375 <212> TYPE: DNA
376 <213> ORGANISM: Homo sapiens
379 <220> FEATURE:
380 <221> NAME/KEY: CDS
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RAW SEQUENCE LISTING ERROR SUMMARY     DATE: 11/15/2005
PATENT APPLICATION:   US/10/555,407     TIME: 10:09:48

Input Set : A:\SeqListing.txt
Output Set: N:\CRF4\11152005\J555407.raw

**<u>Invalid <213> Response:</u>**
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:31,32,33

**VERIFICATION SUMMARY**            DATE: 11/15/2005
PATENT APPLICATION:  **US/10/555,407**      TIME: 10:09:48

Input Set : **A:\SeqListing.txt**
Output Set: **N:\CRF4\11152005\J555407.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date